

B1  
“PILEUP” program (Feng and Doolittle, 1987). Residues that are identical or very similar (K & R; D & E; V & I; M & L) in >8 of the 11 proteins are shaded in dark grey, while less conserved residues (present in > 5/11 proteins) are shaded in light grey. (B) Short stretch of amino acid homology between Bim (SEQ ID NO: 38) and *C. elegans* Ced-4 (SEQ ID NO: 39); this region overlaps with the BH3 region of Bim, indicated by the box.

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After page 89, please insert the printed Sequence.

**REMARKS**

Applicants submit this Amendment to indicate the insertion point for the substitute Sequence Listing filed concurrently herewith. Applicants respectfully request examination on the merits of this application.

Receipt of the initial Office Action on the merits is awaited.

Respectfully submitted,

15 October 2001  
Date

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**Versions with Markings to Show Changes Made**

**IN THE SPECIFICATION**

Please amend the Specification as follows:

**Figure 9** is a diagrammatic representation of the BH3 homology regions in the Bcl-2 family. (A) Amino acid sequences (SEQ ID NOS 27-37, respectively in order of appearance) of the human proteins were aligned with the modified method of Feng and Doolittle used by the GCG "PILEUP" program (Feng and Doolittle, 1987). Residues that are identical or very similar (K & R; D & E; V & I; M & L) in >8 of the 11 proteins are shaded in dark grey, while less conserved residues (present in > 5/11 proteins) are shaded in light grey. (B) Short stretch of amino acid homology between Bim (SEQ ID NO: 38) and *C. elegans* Ced-4 (SEQ ID NO: 39); this region overlaps with the BH3 region of Bim, indicated by the box.